



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/970,518

DATE: 01/25/2002

TIME: 14:02:25

Input Set : N:\Crf3\RULE60\09970518.txt

Output Set: N:\CRF3\01252002\I970518.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hillman, Jennifer L.
6 Shah, Purvi

C--> 8 (ii) TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR

11 (iii) NUMBER OF SEQUENCES: 3

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

15 (B) STREET: 3174 Porter Drive

16 (C) CITY: Palo Alto

17 (D) STATE: CA

18 (E) COUNTRY: USA

19 (F) ZIP: 94304

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette

23 (B) COMPUTER: IBM Compatible

24 (C) OPERATING SYSTEM: DOS

25 (D) SOFTWARE: FastSEQ for Windows Version 2.0

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/970,518

C--> 29 (B) FILING DATE: 03-Oct-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/205,749

34 (B) FILING DATE:

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Billings, Lucy J.

39 (B) REGISTRATION NUMBER: 36,749

40 (C) REFERENCE/DOCKET NUMBER: PF-0249 US

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 415-855-0555

44 (B) TELEFAX: 415-845-4166

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 126 amino acids

50 (B) TYPE: amino acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

54 (vii) IMMEDIATE SOURCE:

55 (A) LIBRARY: THPINOT03

56 (B) CLONE: 2446131

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

W--> 60 Met Ser Tyr Lys Pro Ile Ala Pro Ala Pro Ser Xaa Thr Pro Gly Ser

ENTERED

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61      1              5              10              15
62 Ser Thr Pro Gly Pro Gly Thr Pro Val Pro Thr Gly Ser Val Pro Ser
63              20              25              30
64 Pro Ser Gly Ser Val Pro Gly Ala Gly Ala Pro Phe Arg Pro Leu Phe
65              35              40              45
66 Asn Asp Phe Gly Pro Pro Ser Met Gly Tyr Val Gln Ala Met Lys Pro
67              50              55              60
68 Pro Gly Ala Gln Gly Ser Gln Ser Thr Tyr Thr Asp Leu Leu Ser Val
69 65              70              75              80
70 Ile Glu Glu Met Gly Lys Glu Ile Arg Pro Thr Tyr Ala Gly Ser Lys
71              85              90              95
72 Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile His Ala Arg Ala Leu
73              100              105              110
74 Val Arg Glu Cys Leu Ala Glu Thr Glu Arg Asn Ala Arg Thr
75              115              120              125
77 (2) INFORMATION FOR SEQ ID NO: 2:
78     (i) SEQUENCE CHARACTERISTICS:
79         (A) LENGTH: 667 base pairs
80         (B) TYPE: nucleic acid
81         (C) STRANDEDNESS: single
82         (D) TOPOLOGY: linear
83     (vii) IMMEDIATE SOURCE:
84         (A) LIBRARY: THPINOT03
85         (B) CLONE: 2446131
86     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
87     GGCTGAGCGG CCCCAGCC AACCCCGAG GAGCGCCGG CTGGCGTCCG CCGCGCCCAG      60
88     GAGTTGGGGA TGTCTACAA ACCCATCGCC CCTGCTCCCA GCAKACCCC TGGCTCCAGC      120
89     ACCCTGGGC CGGGACCCC GGTCCCTACA GGAAGCGTCC CGTCGCCGTC GGGCTCAGTG      180
90     CCAGGAGCCG GCGCTCCTT CAGACCGCTG TTTAAGACT TTGGACCGCC TTCCATGGGC      240
91     TACGTGCAGG CGATGAAGCC ACCCGGCGCC CAGGGCTCCC AGAGCACCTA CACGGACCTG      300
92     CTGTCACTCA TAGAGGAGAT GGGCAAAGAG ATCCGGCCTA CCTATGCTGG CAGCAAGAGC      360
93     GCCATGGAGC GCCTGAAGAG AGGTATCATC CATGCCCGGG CCCTAGTCAG AGAGTGCCTG      420
94     GCAGAGACAG AGCGGAACGC CCGCACGTAA CAGGAAGCGC CTCGGCCTCA GCGTCTGGAC      480
95     CTATCCGGCC ACTGCAGAGC ACCCGCTTCT CCCTGGCCTT CATCCCGAGT TGCCTAACC      540
96     ATCCTGGGCT TCCTGTCCTG TGTCCTTGG TGGTCCCCT CCAGGAACCA AGGAGTGGCC      600
97     CTCCAGGTGG CAGCACTAAG GACACCCCC CACAACAAGA GTTAGCAGCG AGGTCCCCAT      660
98     GAGTCCC                                         667
104 (2) INFORMATION FOR SEQ ID NO: 3:
105     (i) SEQUENCE CHARACTERISTICS:
106         (A) LENGTH: 114 amino acids
107         (B) TYPE: amino acid
108         (C) STRANDEDNESS: single
109         (D) TOPOLOGY: linear
110     (vii) IMMEDIATE SOURCE:
111         (A) LIBRARY: GenBank
112         (B) CLONE: 606837
113     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
114     Met Ser Tyr Lys Pro Asn Leu Thr Ala His Met Pro Ala Ala Ala Leu
115     1              5              10              15

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120	Asn	Ala	Gly	Ser	Val	His	Ser	Pro	Ser	Thr	Ser	Met	Ala	Thr	Ser	Ser
121				20				25						30		
122	Gln	Tyr	Arg	Gln	Leu	Leu	Ser	Asp	Tyr	Gly	Pro	Pro	Ser	Leu	Gly	Tyr
123			35					40					45			
124	Thr	Gln	Gly	Thr	Gly	Asn	Ser	Gln	Val	Pro	Gln	Ser	Lys	Tyr	Ala	Glu
125		50					55					60				
126	Leu	Leu	Ala	Ile	Ile	Glu	Glu	Leu	Gly	Lys	Glu	Ile	Arg	Pro	Thr	Tyr
127	65				70					75					80	
128	Ala	Gly	Ser	Lys	Ser	Ala	Met	Glu	Arg	Leu	Lys	Arg	Gly	Ile	Ile	His
129				85					90					95		
130	Ala	Arg	Ser	Leu	Val	Arg	Glu	Cys	Leu	Ala	Glu	Thr	Glu	Arg	Asn	Ala
131				100					105					110		
132	Arg	Ser														

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/970,518

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TIME: 14:02:26

Input Set : N:\Crf3\RULE60\09970518.txt

Output Set: N:\CRF3\01252002\I970518.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:8 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1